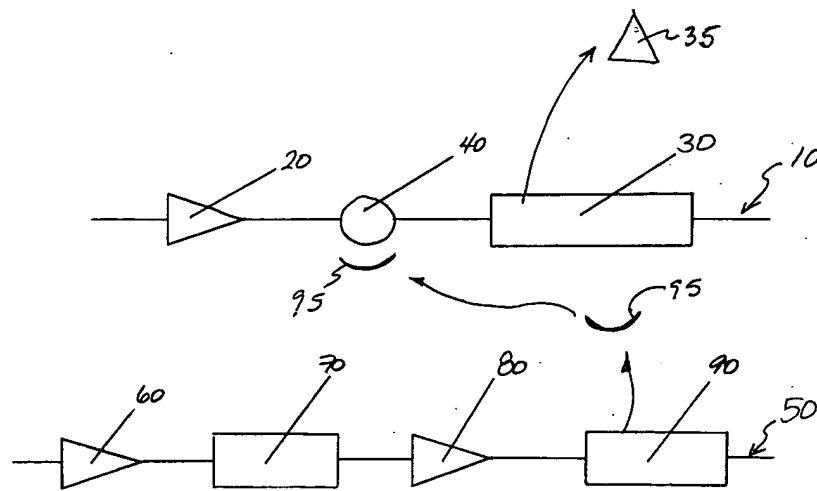
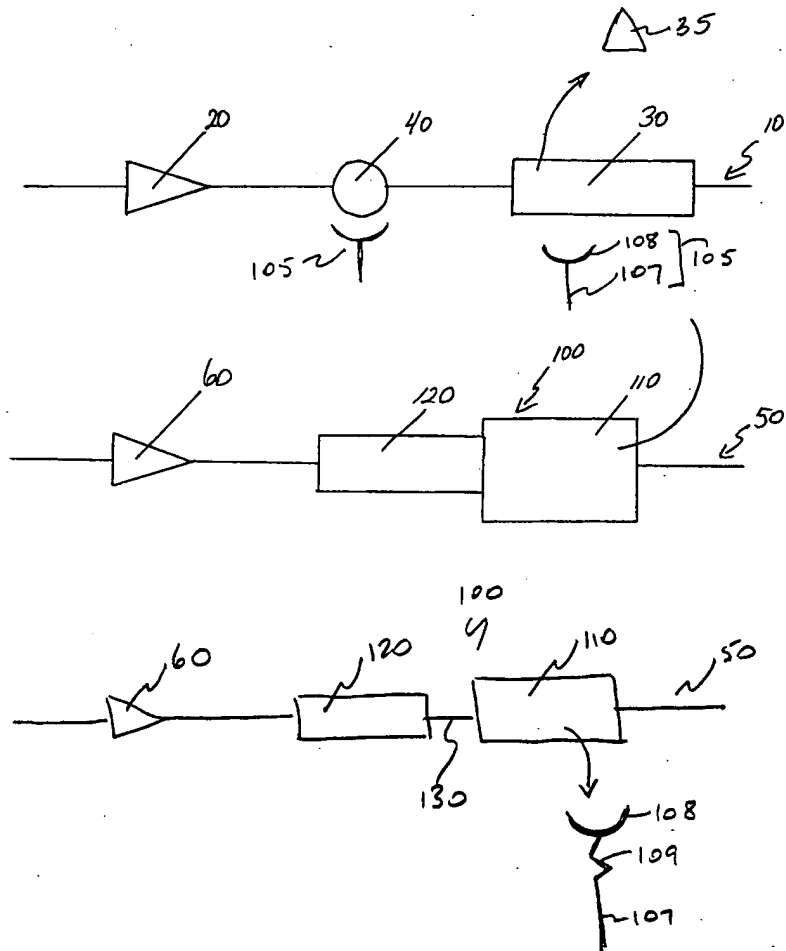


**Fig. 1**



**Fig. 2**



**Fig. 3**

## Fig. 4A

ROS Inverted Repeat  
DNA Binding Sites (Operator sequences)

|                                    |                  |
|------------------------------------|------------------|
| <b>TATATTTCAA-TTTTA-TTGTAATATA</b> | <i>virC/virD</i> |
| ***** ** ** * *** *** **           |                  |
| <b>TATAATTAAAATATTAAGTCGCATT</b>   | <i>ipt</i>       |

## Fig. 4B

Comparison of ROS DNA Binding Site (Operator)  
Sequences

|                  |  |
|------------------|--|
| <i>VirC/VirD</i> | <b>TATATTTCAA</b><br><b>TATATTACAA</b> |
| <i>ipt</i>       | <b>TATAATTAAA</b><br><b>AATGCGACAG</b> |
|                  | <b>TATAHTtCAA</b><br><b>a g gaa g</b>  |
| <b>Consensus</b> | <b>WATDHWKMAR</b>                      |

1    - - - - - - - - - - ATGACGGAACTGCATACGGTAACGC    ROS GENE  
1    GCGGATCCCCGGGTATGACTGAGACTGCTTACGGTAACGC    ROS.SYN.seq

27    CCAGGATCTGCTGGTCGAACTGACGGCGGATATTGTGGCT    ROS GENE  
41    TCAGGATCTTCTTGTGTGAGCTTACTGCTGATATCGTTGCT    ROS.SYN.seq

67    GCCATATGTTAGCAACCACGTCGTTCCGGTAACTGAGCTTC    ROS GENE  
81    GCTTACGTTTCTAACCACGTTGTTCTTGTACTGAGCTTC    ROS.SYN.seq

107    CCGGCCTTATTTTCGGATGTTTCATACGGCACTCAGCGGAAC    ROS GENE  
121    CTGGACTTATCTCTGATGTTTCATACATGCACTTTCCTGGAACT    ROS.SYN.seq

147    ATCGGCACCGGCATCGGTGGCGGTCAATGTTGAAAAGCAG    ROS GENE  
161    ATCTGCTTCCGCTTCTGTGTGCTGTTTAACTGTGAGAAAGCAG    ROS.SYN.seq

187    AAGCCTGCTGTGTCGGTTCGCAAGTCGGTTCAGGACGATC    ROS GENE  
201    AAGCCTGCTGTTCCTGTTCTGTAAAGTCTGTTCAAGATGATC    ROS.SYN.seq

227    ATATCGTCTGTTTGGAATGTGGTGGCTCGTTCAAGTCGCT    ROS GENE  
241    ATATCGTTTGTGTTGGAGTGTGGTGGTTCTTTTCAAGTCTCT    ROS.SYN.seq

267    CAAACGCCACCTGACGACGCAACACAGCATGACGCCGGAAC    ROS GENE  
281    CAAGCGTCACTTACTACTCATCACTCTATGACTCCAGAG    ROS.SYN.seq

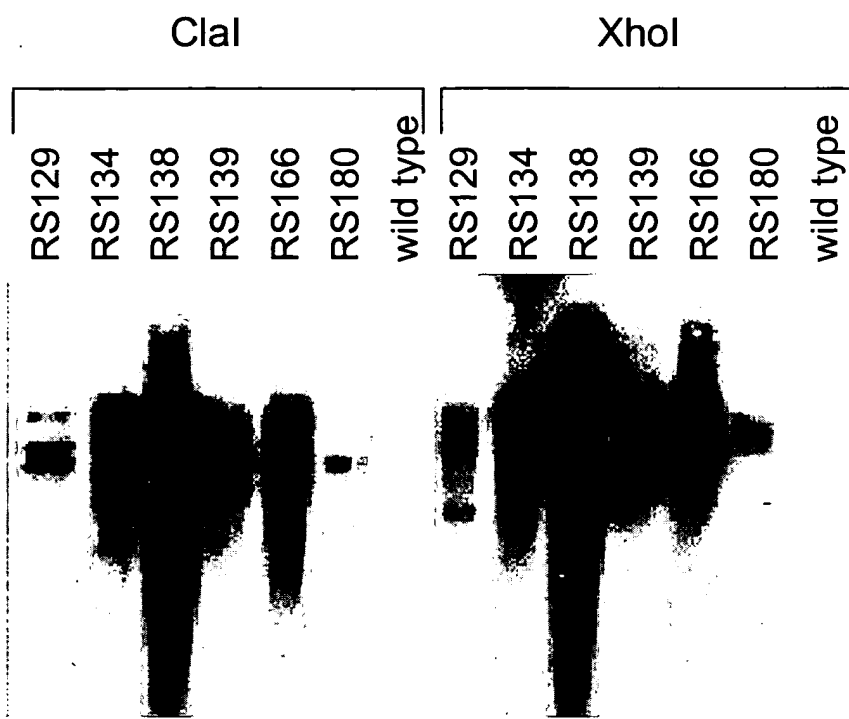
307    GAATATCGCGAAAAATGGGATCTGCCGGTCGATTATCCGA    ROS GENE  
321    GAGTATAGAAGAGTGGGATCTTCTGTGTTGATTACCCCTA    ROS.SYN.seq

347    TGGTTGCTCCCGCCTATGCCGAAGCCCGTTTCGCGGCTCGC    ROS GENE  
361    TGGTTGCTCTGCTTACGCTGAGGCTTCGTTCTCGTCTCGC    ROS.SYN.seq

387    CAAGGAAATGGGTCTCGGTCAAGCGCCGCAAGGCGAACCCT    ROS GENE  
401    TAAAGGAGATGGGTCTCGGTCAAGCGTCGTAAAGCTAACCCT    ROS.SYN.seq

427    - - - - - - - - - - TGA    ROS GENE  
441    CCAAAAAAGAAAGCGTAAGGCTGAGAGCTCGC    ROS.SYN.seq

Fig. 4C



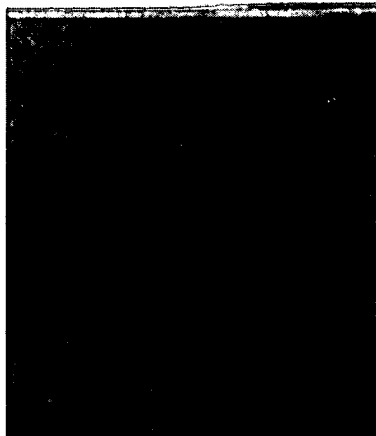
**Fig. 4D**

p74-101

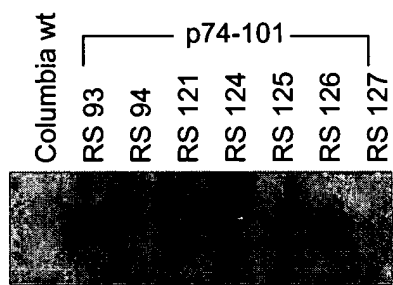
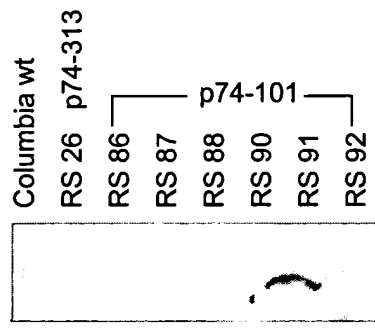
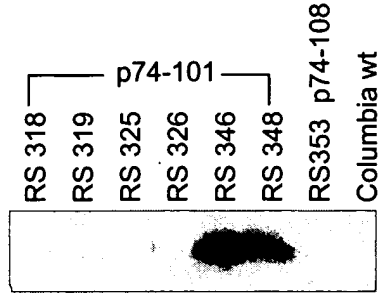
RS 91

RS 93

RS 121



**Fig. 4E**



**Fig. 4F**



Columbia wt

pB1121



p74-501



buffer

**Fig. 4G**

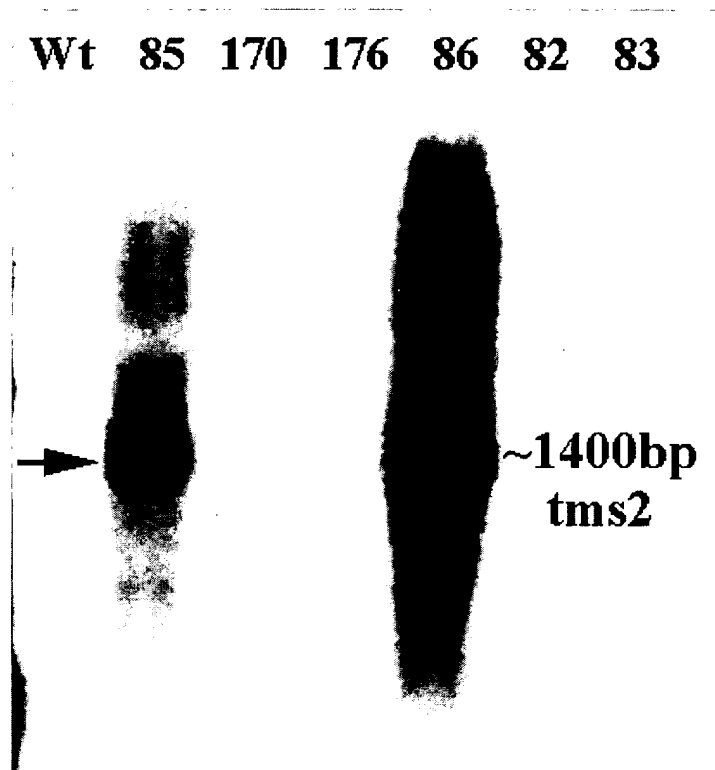
1    - - - - - - - - - - ATGTCTAGATTAGATAAAAGTAAAGTGA WttetrepORF.s  
1    GGTACCGAGAAAATGTCTAGATTAGATAAAAGTAAAGTGA TetR.Syn.seq  
  
29   TTAACAGCGCATTAGAGCTGCTTAATGAGGTCGGAATCGA WttetrepORF.s  
41   TTAACAGCGCATTAGAGCTGCTTAATGAGGTCGGAATCGA TetR.Syn.seq  
  
69   AGGCCTAACAAACCCGTAAACTTGCGCAGAAAGCTCGGGGTA WttetrepORF.s  
81   GGGCTTAACGACCCGTAAACTCGCGCAGAAAGCTAGGA GTA TetR.Syn.seq  
  
109   GAGCAGCCTACATTGTATTGGCATGTAAAAAATAAGCGGG WttetrepORF.s  
121   GAGCAGCCTACGTTGTACTTGGCATGTTAAGAA CAAGCGGG TetR.Syn.seq  
  
149   CCCTGCTCGACGCGTTAGCCATTGAGATGTTAGATAGGCA WttetrepORF.s  
161   CTTTGCTCGACGCCCTCGCGATTGAGATGTTAGACAGGCA TetR.Syn.seq  
  
189   CCATACTCACTTTTGCCCTTTAGAAGGGGAAGCTGGCAA WttetrepORF.s  
201   CCATACTCACTTCTGCCCTCTCGAAGGGGAGAGCTGGCAA TetR.Syn.seq  
  
229   GATTTTTTACGTAAATAACGCTAAAAGTTTATAGATGTGCTT WttetrepORF.s  
241   GATTTCTCTCGTAAACAACGCTAAGTCTTCTAGATGTGCTC TetR.Syn.seq  
  
269   TACTAAGTCATCGCGATGGAGCAAAAGTACATTTAGGTAC WttetrepORF.s  
281   TCTTA TCCATCGCGACGGAGCAAAAGTT CATCTGGGTAC TetR.Syn.seq  
  
309   ACGGCCTACAGAAAAACAGTATGAAACTCTCGAAAAATCAA WttetrepORF.s  
321   ACGGCCTACAGAGAAACAGTATGAGACTCTCGAAAAATCAA TetR.Syn.seq  
  
349   TTAGCCTTTTATAGCCAACAAGGTTTTCCTCACTAGAGAAATG WttetrepORF.s  
361   CTGGCCTTTCTGTGCCAACAGGGTTTCTCACTAGAGAAATG TetR.Syn.seq  
  
389   CATTATATGCACTCAGCGCTGTGGGGCATTTTACTTTAGG WttetrepORF.s  
401   CGCTTTTACGCACCTCTCAGCTGTGGGGCATTTTACTCTTGG TetR.Syn.seq  
  
429   TTGCGTATTGGAAGATCAAGAGCATCAAGTCGCTAAAGAA WttetrepORF.s  
441   TTGCGTTTTGGA GGATCAAGAGCATCAAGTCGCTAAGGAA TetR.Syn.seq  
  
469   GAAAGGGAAACA CTA CTA CTGATAGTATGCCGCCAT TAT WttetrepORF.s  
481   GAGAGGGAAACA CTA CTA CTGATAGTATGCCGCCA CTT C TetR.Syn.seq  
  
509   TACGACAAGCTATCGAATTATTTGATCACCAAGGTGCAGA WttetrepORF.s  
521   TTCGACAAGCCATCGAACTTTTGTGATCACCAAGGGTGCAGA TetR.Syn.seq  
  
549   GCCAGCCTTCTTATTCGGCCTTGAAATTGATCATATGCGGA WttetrepORF.s  
561   GCCAGCCTTCTTGTTTCGGCCTTGAAATTGATCATATGCGGA TetR.Syn.seq  
  
589   TTAGAAAAACAACCTTAAATGTGAA - - - - - WttetrepORF.s  
601   TTGGAAAAGCAGCTTAAATGTGAA TCGGGGTCTCTTAAAGC TetR.Syn.seq  
  
613   - - - - - - - AGTG - - - GGTCT - - - - - TAA WttetrepORF.s  
641   CAAAAAAGAAGCGTAAAGGTCTGACTTAAAGTGAATCGA T T TetR.Syn.seq

**Fig. 5**

|     |   |        |
|-----|---|--------|
| 1   | MTETAYGNAQDILLVELTADIVAAVVSNNHVVVTELPGLISDVHTALSGTS | SynROS |
| 1   | MTETAYGNAQDILLVELTADIVAAVVSNNHVVVTELPGLISDVHTALSGTS | Wtros  |
| 51  | APASVAVNVEKQKPAVSVRKS VQDDHIVCLECGGSFKSLKRHLTTHHSMT | SynROS |
| 51  | APASVAVNVEKQKPAVSVRKS VQDDHIVCLECGGSFKSLKRHLTTHHSMT | Wtros  |
| 101 | PEEYREKWDLPVDYPMVAPAYAEARSRLAKEMGLGQRRKANR          | SynROS |
| 101 | PEEYREKWDLPVDYPMVAPAYAEARSRLAKEMGLGQRRKANR          | Wtros  |

Fig. 6





**Fig. 8**

## Repressor Construct



## Reporter Constructs

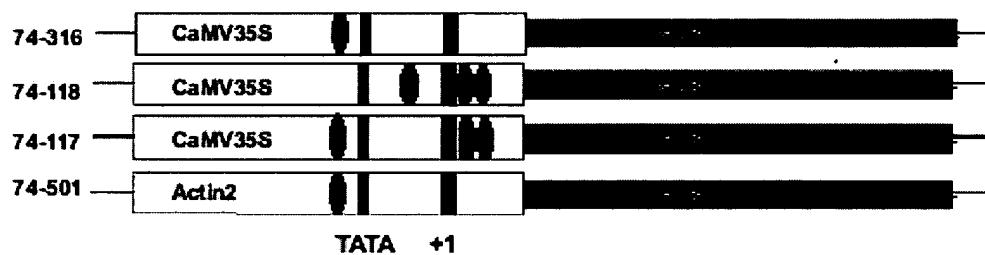
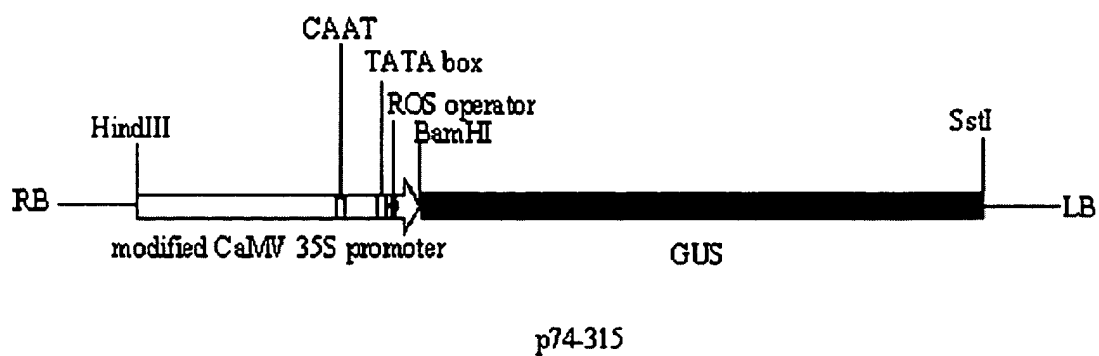
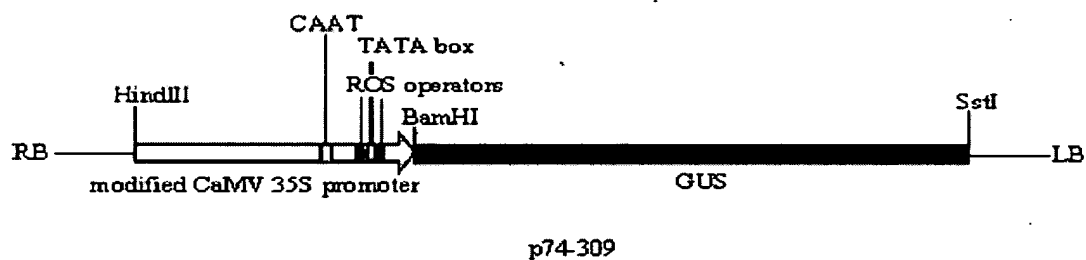


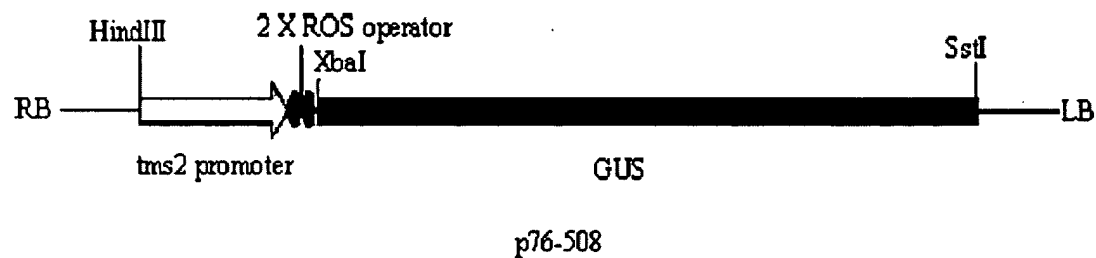
Fig. 9A



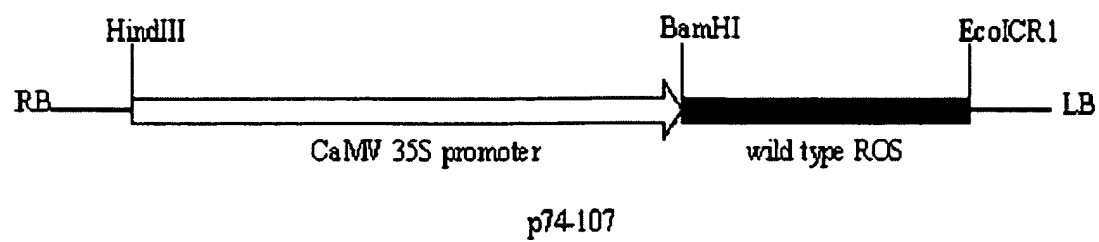
**Fig. 9B**



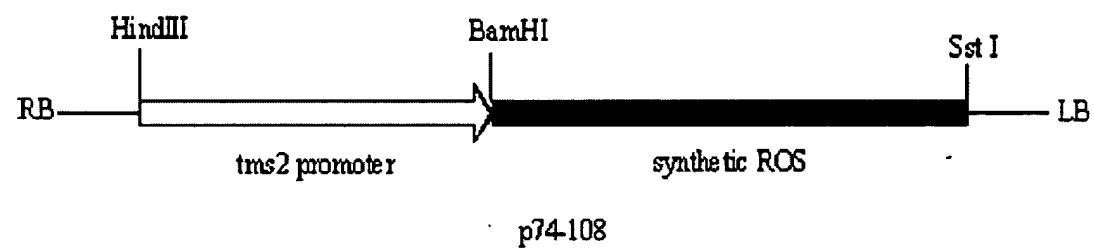
**Fig. 9C**



**Fig. 9D**

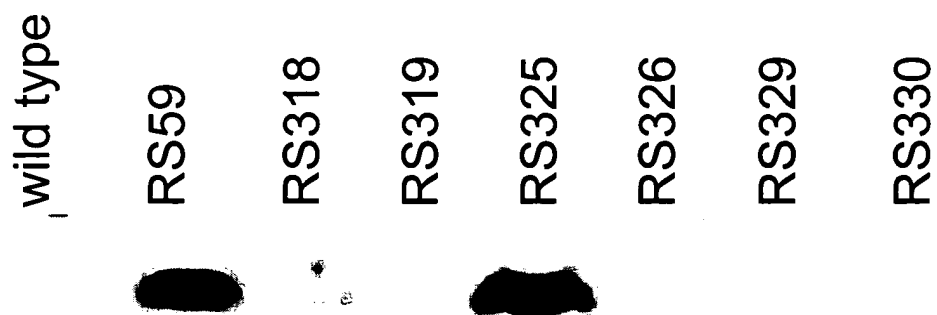


**Fig. 9E**

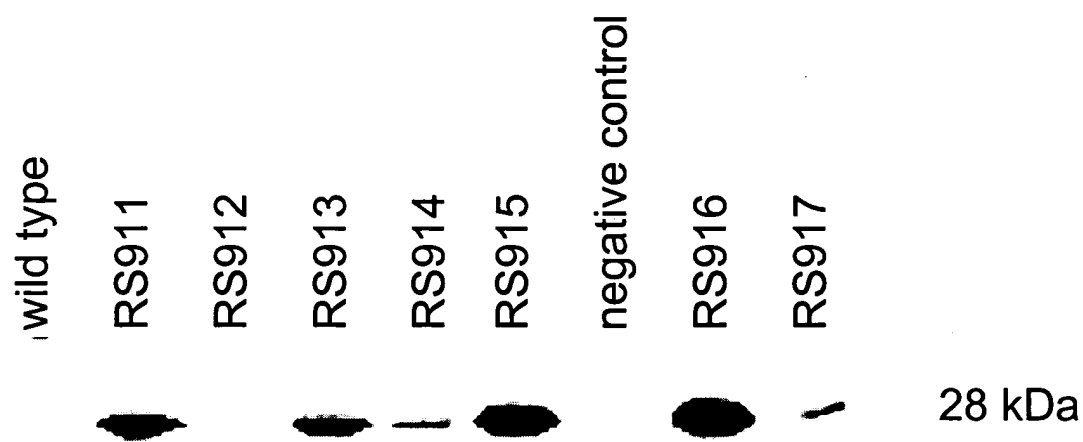


**Fig. 9F**

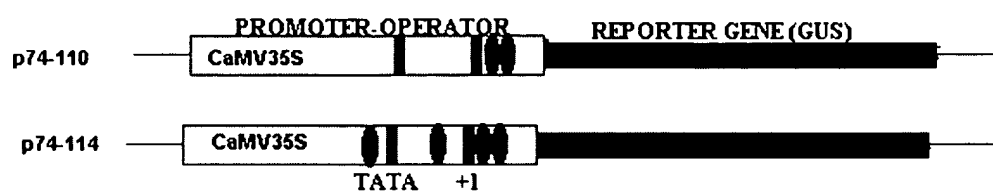




**Fig. 10A**



**Fig. 10B**

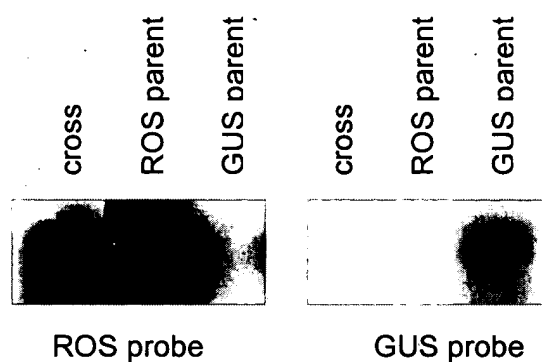


**Fig. 11**

GUS assay

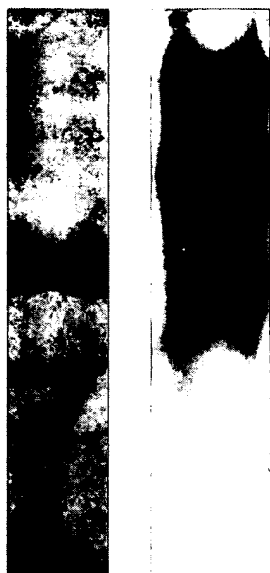
cross    ROS parent    GUS parent

**Fig. 12A**



Northern blots

**Fig. 12B**



GUS probe ROS probe

Southern blot

**Fig. 12C**

Fig. 13A

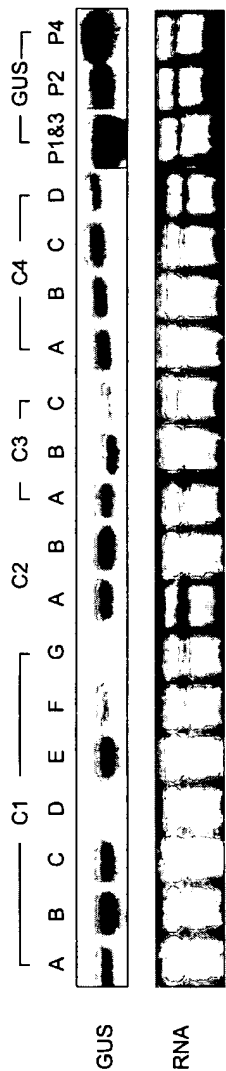


Fig. 13B

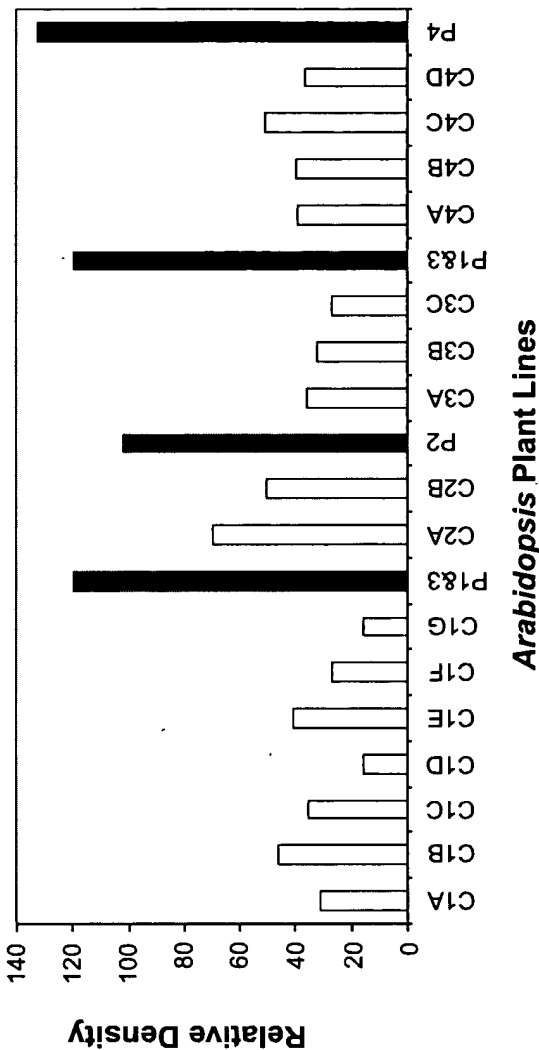
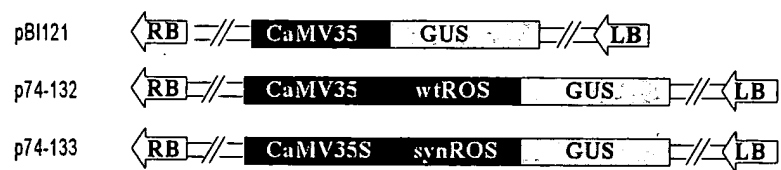
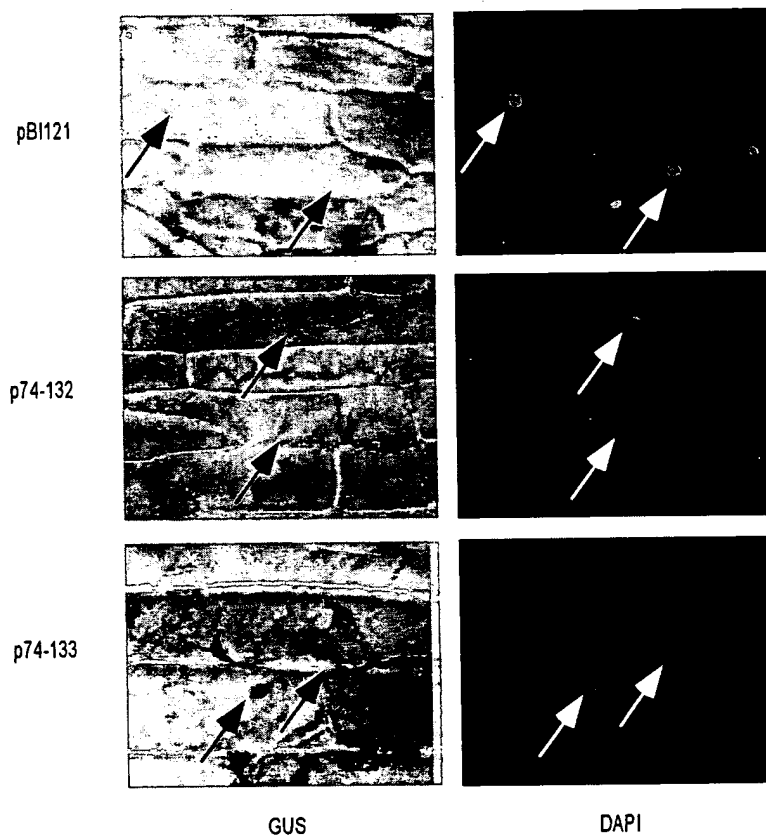


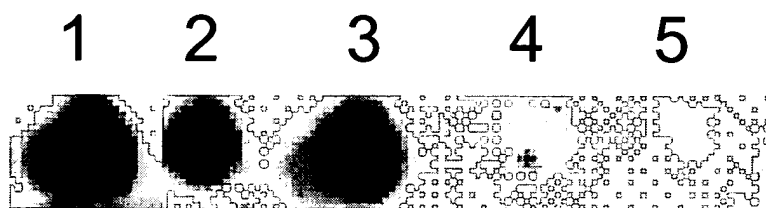
Fig. 13

**Fig. 14A**

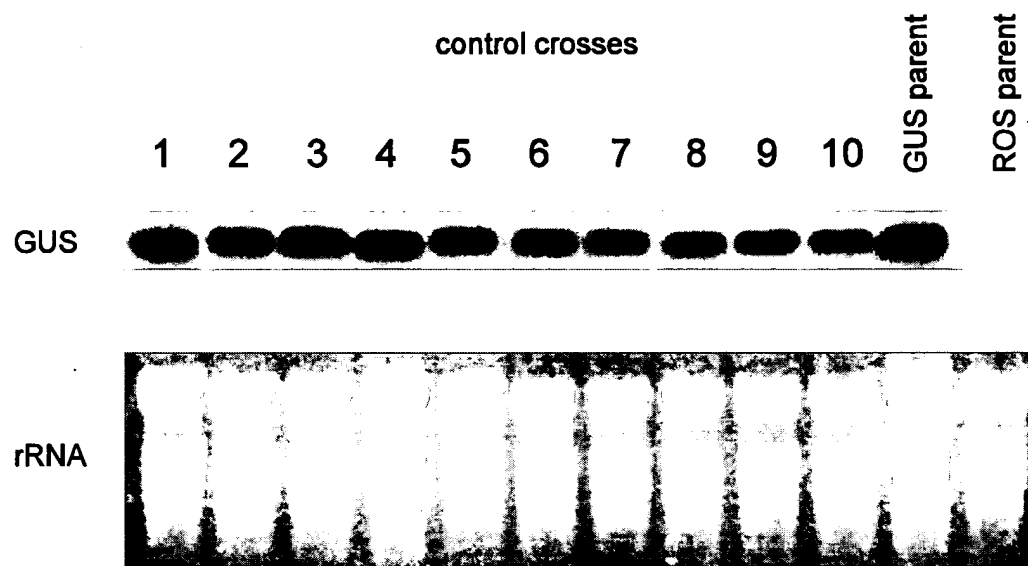


**Fig. 14B**

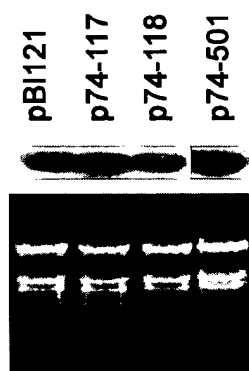




**Fig. 15**



**Fig. 16A**



**Fig. 16B**



Fig. 17A

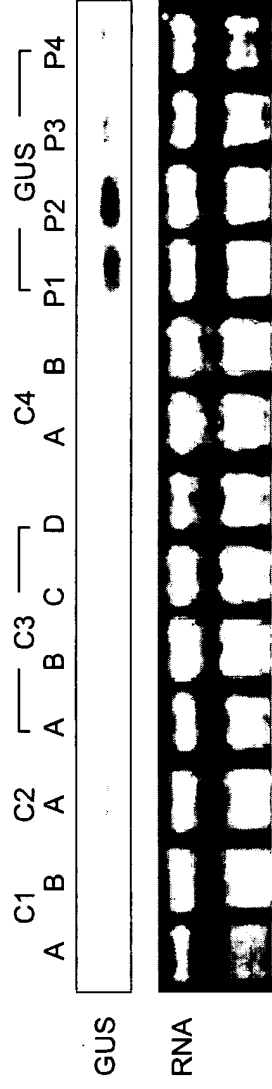


Fig. 17B

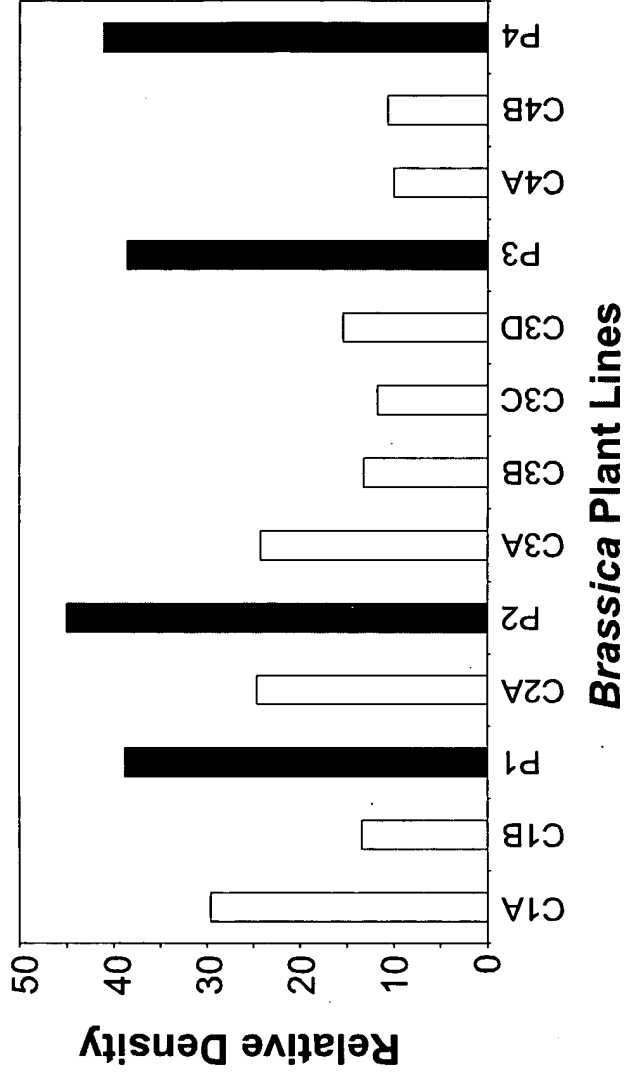


Fig. 17